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Patent and Trademark Office**

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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.
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09/298,523 04/23/99 BRILES

D 454312-3140

EXAMINER

HM12/0228

WILLIAM S FROMMER
FROMMER LAWRENCE & HAUG LLP
745 FIFTH AVENUE
NEW YORK NY 10151

MINNIFIELD, N

ART UNIT

PAPER NUMBER

1645

DATE MAILED:

02/28/01

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trademarks



UNITED STATES DEPARTMENT OF COMMERCE
Patent and Trademark Office

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Washington, D.C. 20231

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.
09/298523	04/23/99	BRILES ET AL	454312-3140

p

p

EXAMINER	
MINNIFIELD	
ART UNIT	PAPER NUMBER
1645	10

p

p

DATE MAILED:

Commissioner of Patents

Please find below a communication from the EXAMINER in charge of this application.

1. The communication filed November 11, 2000 is not fully responsive to the Office communication mailed June 19, 2000 for the reason(s) set forth on the attached Notice To Comply With The Sequence Rules or CRF Diskette Problem Report. Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825) before the application can be examined under 35 U.S.C. §§ 131 and 132. Direct the reply to the undersigned. Applicant is requested to return a copy of the attached CRF Diskette Problem Report with the reply.

Since the above-mentioned reply appears to be *bona fide* attempt to comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825), applicant is given a TIME PERIOD of **ONE (1) MONTH** from the mailing date of this communication within which to correct the deficiency so as to comply with the sequence rules (37 CFR 1.821 - 1.825) in order to avoid abandonment of the application under 37 CFR 1.821(g). **EXTENSIONS OF THIS TIME PERIOD MAY BE GRANTED UNDER 37 CFR 1.136(a).**

2. Any inquiry concerning this communication or earlier communications from the examiner should be directed to N. M. Minnifield whose telephone number is (703) 305-3394. The examiner can normally be reached on Monday-Thursday from 7:00 AM-4:30 PM. The examiner can also be reached on alternate Fridays.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Lynette R. F. Smith, can be reached on (703) 308-3909. The fax phone number for TECH CENTER 1600 is (703) 308-4556.

Any inquiry of a general nature or relating to the status of this application should be directed to the TECH CENTER 1600 receptionist whose telephone number is (703) 308-0196.

N. M. Minnifield

February 27, 2001

substitute PTOL90


NITA MINNIFIELD
PRIMARY EXAMINER

Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/298,523A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PATENTIN

RECEIVED

NOV 28 2000

TELEPHONE 1600/2900

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid-number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
&400> sequence id number
000
- 10 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism (NEW RULES) Sequence(s) are missing this mandatory field or its response.
- 12 Use of <220>Feature (NEW RULES) Sequence(s) are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

N. Minnifield

RECEIVED Page 1 of 7

NOV 28 2000

FILED : 021600/2900

1645

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/298,523A

DATE: 11/16/2000
TIME: 18:17:02

Input Set : A:\Brilesal.app
Output Set: N:\CRF3\11162000\I298523A.raw

Does Not Comply
Corrected Diskette Needed

P.6

```
3 <110> APPLICANT: BRILES et al.
5 <120> TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC), EPITOPIC REGIONS
6 AND STRAINS THEREOF AND USES THEREFOR
8 <130> FILE REFERENCE: 454312-3140
10 <140> CURRENT APPLICATION NUMBER: 09/298,523A
11 <141> CURRENT FILING DATE: 1999-04-23
13 <160> NUMBER OF SEQ ID NOS: 78
15 <170> SOFTWARE: PatentIn Ver. 2.1
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 691
19 <212> TYPE: PRT
20 <213> ORGANISM: Streptococcus pneumoniae
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27 20 25 30
29 Gly Val Val His Ala Glu Gly Val Arg Ser Gly Asn Asn Leu Thr Val
30 35 40 45
32 Thr Ser Ser Gly Gln Asp Ile Ser Lys Lys Tyr Ala Asp Glu Val Glu
33 50 55 60
35 Ser His Leu Glu Ser Ile Leu Lys Asp Val Lys Lys Asn Leu Lys Lys
36 65 70 75 80
38 Val Gln His Thr Gln Asn Val Gly Leu Ile Thr Lys Leu Ser Glu Ile
39 85 90 95
41 Lys Lys Lys Tyr Leu Tyr Asp Leu Lys Val Asn Val Leu Ser Glu Ala
42 100 105 110
44 Glu Leu Thr Ser Lys Thr Lys Glu Thr Lys Glu Lys Leu Thr Ala Thr
45 115 120 125
47 Phe Glu Gln Phe Lys Lys Asp Thr Leu Pro Thr Glu Pro Glu Lys Lys
48 130 135 140
50 Val Ala Glu Ala Gln Lys Lys Val Glu Glu Ala Lys Lys Lys Ala Glu
51 145 150 155 160
53 Asp Gln Lys Glu Lys Asp Arg Arg Asn Tyr Pro Thr Ile Thr Tyr Lys
54 165 170 175
56 Thr Leu Glu Leu Glu Ile Ala Glu Ser Asp Val Glu Val Lys Lys Ala
57 180 185 190
59 Glu Leu Glu Leu Val Lys Val Lys Ala Lys Glu Ser Gln Asp Glu Glu
60 195 200 205
62 Lys Ile Lys Gln Ala Glu Ala Glu Val Glu Ser Lys Gln Ala Glu Ala
63 210 215 220
65 Thr Arg Leu Lys Lys Ile Lys Thr Asp Arg Glu Glu Ala Lys Arg Lys
66 225 230 235 240
68 Ala Asp Ala Lys Leu Lys Glu Ala Val Glu Lys Asn Val Ala Thr Ser
69 245 250 255
71 Glu Gln Asp Lys Pro Lys Arg Arg Ala Lys Arg Gly Val Ser Gly Glu
72 260 265 270
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/298,523A

DATE: 11/16/2000

TIME: 18:17:02

Input Set : A:\Brilesal.app

Output Set: N:\CRF3\11162000\I298523A.raw

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NOV 28 2000

TECH CENTER 1600/2900

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74 Leu Ala Thr Pro Asp Lys Lys Glu Asn Asp Ala Lys Ser Ser Asp Ser
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77 Ser Val Gly Glu Glu Thr Leu Pro Ser Pro Ser Leu Asn Met Ala Asn
78          290          295          300
80 Glu Ser Gln Thr Glu His Arg Lys Asp Val Asp Glu Tyr Ile Lys Lys
81 305          310          315          320
83 Met Leu Ser Glu Ile Gln Leu Asp Arg Arg Lys His Thr Gln Asn Val
84          325          330          335
86 Asn Leu Asn Ile Lys Leu Ser Ala Ile Lys Thr Lys Tyr Leu Tyr Glu
87          340          345          350
89 Leu Ser Val Leu Lys Glu Asn Ser Lys Lys Glu Glu Leu Thr Ser Lys
90          355          360          365
92 Thr Lys Ala Glu Leu Thr Ala Ala Phe Glu Gln Phe Lys Lys Asp Thr
93          370          375          380
95 Leu Lys Pro Glu Lys Lys Val Ala Glu Ala Glu Lys Lys Val Glu Glu
96 385          390          395          400
98 Ala Lys Lys Lys Ala Lys Asp Gln Lys Glu Glu Asp Arg Arg Asn Tyr
99          405          410          415
101 Pro Thr Asn Thr Tyr Lys Thr Leu Glu Leu Glu Ile Ala Glu Ser Asp
102          420          425          430
104 Val Lys Val Lys Glu Ala Glu Leu Glu Leu Val Lys Glu Ala Asn
105          435          440          445
107 Glu Ser Arg Asn Glu Glu Lys Ile Lys Gln Ala Lys Glu Lys Val Glu
108          450          455          460
110 Ser Lys Lys Ala Glu Ala Thr Arg Leu Glu Lys Ile Lys Thr Asp Arg
111 465          470          475          480
113 Lys Lys Ala Glu Glu Glu Ala Lys Arg Lys Ala Glu Glu Ser Glu Lys
114          485          490          495
116 Lys Ala Ala Glu Ala Lys Gln Lys Val Asp Ala Glu Glu Tyr Ala Leu
117          500          505          510
119 Glu Ala Lys Ile Ala Glu Leu Glu Tyr Glu Val Gln Arg Leu Glu Lys
120          515          520          525
122 Glu Leu Lys Glu Ile Asp Glu Ser Asp Ser Glu Asp Tyr Leu Lys Glu
123          530          535          540
125 Gly Leu Arg Ala Pro Leu Gln Ser Lys Leu Asp Thr Lys Lys Ala Lys
126 545          550          555          560
128 Leu Ser Lys Leu Glu Glu Leu Ser Asp Lys Ile Asp Glu Leu Asp Ala
129          565          570          575
131 Glu Ile Ala Lys Leu Glu Val Gln Leu Lys Asp Ala Glu Gly Asn Asn
132          580          585          590
134 Asn Val Glu Ala Tyr Phe Lys Glu Gly Leu Glu Lys Thr Thr Ala Glu
135          595          600          605
137 Lys Lys Ala Glu Leu Glu Lys Ala Glu Ala Asp Leu Lys Lys Ala Val
138          610          615          620
140 Asp Glu Pro Glu Thr Pro Ala Pro Ala Pro Gln Pro Ala Pro Ala Pro
141 625          630          635          640
143 Glu Lys Pro Ala Glu Lys Pro Ala Pro Ala Pro Glu Lys Pro Ala Pro
144          645          650          655
146 Ala Pro Glu Lys Pro Ala Pro Ala Pro Glu Lys Pro Ala Pro Ala Pro

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RAW SEQUENCE LISTING DATE: 11/16/2000
 PATENT APPLICATION: US/09/298,523A TIME: 18:17:02

Input Set : A:\Brilesal.app
 Output Set: N:\CRF3\11162000\I298523A.raw

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147          660          665          670
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152 Pro Lys Thr
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157 <211> LENGTH: 707
158 <212> TYPE: PRT
159 <213> ORGANISM: Streptococcus pneumoniae
161 <400> SEQUENCE: 2
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165 Phe Ser Ile Gly Val Ala Ser Val Ala Val Ala Ser Leu Phe Leu Gly
166          20          25          30
168 Gly Val Val His Ala Glu Gly Val Arg Ser Gly Asn Asn Leu Thr Val
169          35          40          45
171 Thr Ser Ser Gly Gln Asp Ile Ser Lys Lys Tyr Ala Asp Glu Val Glu
172   50          55          60
174 Ser His Leu Glu Ser Ile Leu Lys Asp Val Lys Lys Asn Leu Lys Lys
175 65          70          75          80
177 Val Gln His Thr Gln Asn Val Gly Leu Ile Thr Lys Leu Ser Glu Ile
178          85          90          95
180 Lys Lys Lys Tyr Leu Tyr Asp Leu Lys Val Asn Val Leu Ser Glu Ala
181          100         105         110
183 Glu Leu Thr Ser Lys Thr Lys Glu Thr Lys Glu Lys Leu Thr Ala Thr
184          115         120         125
186 Phe Glu Gln Phe Lys Lys Asp Thr Leu Pro Thr Glu Pro Glu Lys Lys
187          130         135         140
189 Val Ala Glu Ala Gln Lys Lys Val Glu Glu Ala Lys Lys Lys Ala Glu
190 145          150         155         160
192 Asp Glu Lys Glu Lys Asp Arg Arg Asn Tyr Pro Thr Ile Thr Tyr Lys
193          165         170         175
195 Thr Leu Glu Leu Glu Ile Ala Glu Ser Asp Val Glu Val Lys Lys Ala
196          180         185         190
198 Glu Leu Glu Leu Val Lys Val Lys Ala Lys Glu Ser Gln Asp Glu Glu
199          195         200         205
201 Lys Ile Lys Gln Ala Glu Ala Glu Val Glu Ser Lys Gln Ala Glu Ala
202          210         215         220
204 Thr Arg Leu Lys Lys Ile Lys Thr Asp Arg Glu Glu Ala Lys Arg Lys
205 225         230         235         240
207 Ala Asp Ala Lys Leu Lys Glu Ala Val Glu Lys Asn Val Ala Thr Ser
208          245         250         255
210 Glu Gln Asp Lys Pro Lys Arg Arg Ala Lys Arg Gly Val Ser Gly Glu
211          260         265         270
213 Leu Ala Thr Pro Asp Lys Lys Glu Asn Asp Ala Lys Ser Ser Asp Ser
214          275         280         285
216 Ser Val Gly Glu Glu Thr Leu Pro Ser Pro Ser Leu Asn Met Ala Asn
217          290         295         300
219 Glu Ser Gln Thr Glu His Arg Lys Asp Val Asp Glu Tyr Ile Lys Lys

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RAW SEQUENCE LISTING

DATE: 11/16/2000

PATENT APPLICATION: US/09/298,523A

TIME: 18:17:02

Input Set : A:\Brilesal.app

Output Set: N:\CRF3\11162000\I298523A.raw

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220 305          310          315          320
222 Met Leu Ser Glu Ile Gln Leu Asp Gly Arg Lys His Thr Pro Asn Val
223          325          330          335
225 Asn Leu Asn Ile Lys Leu Ser Ala Ile Lys Thr Lys Tyr Leu Tyr Glu
226          340          345          350
228 Leu Ser Val Leu Lys Glu Asn Ser Lys Lys Glu Glu Leu Thr Ser Lys
229          355          360          365
231 Thr Lys Ala Glu Leu Thr Ala Ala Phe Glu Gln Phe Lys Lys Asp Thr
232          370          375          380
234 Leu Lys Pro Glu Lys Lys Val Ala Glu Ala Glu Lys Lys Val Glu Glu
235 385          390          395          400
237 Ala Lys Lys Lys Ala Lys Asp Gln Lys Glu Glu Asp Arg Arg Asn Tyr
238          405          410          415
240 Pro Thr Asn Thr Tyr Lys Thr Leu Glu Leu Glu Ile Ala Glu Ser Asp
241          420          425          430
243 Val Lys Val Lys Glu Ala Glu Leu Glu Leu Val Lys Glu Glu Ala Asn
244          435          440          445
246 Glu Ser Arg Asn Glu Glu Lys Ile Lys Gln Ala Lys Glu Lys Val Glu
247          450          455          460
249 Ser Lys Lys Ala Glu Ala Thr Arg Leu Glu Lys Ile Lys Thr Asp Arg
250 465          470          475          480
252 Lys Lys Ala Glu Glu Ala Lys Arg Lys Ala Glu Glu Ser Glu Lys
253          485          490          495
255 Lys Ala Ala Glu Ala Lys Gln Lys Val Asp Ala Glu Glu Tyr Ala Leu
256          500          505          510
258 Glu Ala Lys Ile Ala Glu Leu Glu Tyr Glu Val Gln Arg Leu Glu Lys
259          515          520          525
261 Glu Leu Lys Glu Ile Asp Glu Ser Asp Ser Glu Asp Tyr Leu Lys Glu
262          530          535          540
264 Gly Leu Arg Ala Pro Leu Gln Ser Lys Leu Asp Thr Lys Lys Ala Lys
265 545          550          555          560
267 Leu Ser Lys Leu Glu Leu Ser Asp Lys Ile Asp Glu Leu Asp Ala
268          565          570          575
270 Glu Ile Ala Lys Leu Glu Val Gln Leu Lys Asp Ala Glu Gly Asn Asn
271          580          585          590
273 Asn Val Glu Ala Tyr Phe Lys Glu Gly Leu Glu Lys Thr Thr Ala Glu
274          595          600          605
276 Lys Lys Ala Glu Leu Glu Lys Ala Glu Ala Asp Leu Lys Lys Ala Val
277          610          615          620
279 Asp Glu Pro Glu Thr Pro Ala Pro Ala Pro Gln Pro Ala Pro Ala Pro
280 625          630          635          640
282 Glu Lys Pro Ala Glu Lys Pro Ala Pro Ala Pro Ala Pro Glu Lys Pro
283          645          650          655
285 Ala Pro Ala Pro Glu Lys Pro Ala Pro Ala Pro Glu Lys Pro Ala Pro
286          660          665          670
288 Ala Pro Glu Lys Pro Ala Pro Ala Pro Glu Lys Pro Ala Pro Ala Pro
289          675          680          685
291 Glu Lys Pro Ala Pro Ala Pro Glu Lys Pro Ala Pro Ala Thr Pro Lys
292          690          695          700

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RAW SEQUENCE LISTING

DATE: 11/16/2000

PATENT APPLICATION: US/09/298,523A

TIME: 18:17:02

Input Set : A:\Brilesal.app

Output Set: N:\CRF3\11162000\I298523A.raw

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294 Pro Glu Thr
295 705
298 <210> SEQ ID NO: 3
299 <211> LENGTH: 711
300 <212> TYPE: PRT
301 <213> ORGANISM: Streptococcus pneumoniae
303 <400> SEQUENCE: 3
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305 1 5 10 15
307 Phe Ser Ile Gly Val Ala Ser Val Val Val Ala Ser Leu Val Met Gly
308 20 25 30
310 Ser Val Val His Ala Thr Glu Asn Glu Gly Ile Thr Gln Val Ala Thr
311 35 40 45
313 Ser Tyr Asn Lys Ala Asn Glu Ser Gln Thr Glu His Arg Lys Ala Ala
314 50 55 60
316 Lys Gln Val Asp Glu Asp Ile Lys Lys Met Leu Ser Glu Ile Gln Glu
317 65 70 75 80
319 Tyr Ile Lys Lys Met Leu Ser Glu Ile Gln Leu Asp Lys Arg Lys His
320 85 90 95
322 Thr Gln Asn Val Asn Leu Asn Arg Lys Leu Ser Ala Ile Gln Thr Lys
323 100 105 110
325 Tyr Leu Tyr Glu Leu Arg Val Leu Lys Glu Lys Ser Lys Lys Glu Glu
326 115 120 125
328 Leu Thr Ser Lys Thr Lys Lys Glu Leu Asp Ala Ala Phe Glu Lys Phe
329 130 135 140
331 Lys Lys Glu Glu Pro Glu Leu Thr Lys Lys Leu Ala Glu Ala Lys Gln
332 145 150 155 160
334 Lys Ala Lys Ala Gln Lys Glu Glu Asp Phe Arg Asn Tyr Pro Thr Asn
335 165 170 175
337 Thr Tyr Lys Thr Leu Glu Leu Glu Ile Ala Glu Phe Asp Val Lys Val
338 180 185 190
340 Lys Glu Ala Glu Leu Glu Leu Val Lys Glu Glu Ala Lys Pro Arg Asn
341 195 200 205
343 Glu Glu Lys Ile Lys Gln Ala Lys Ala Lys Val Glu Ser Lys Lys Ala
344 210 215 220
346 Glu Ala Thr Arg Leu Glu Glu Ile Lys Thr Glu Arg Lys Lys Ala Glu
347 225 230 235 240
349 Glu Glu Ala Lys Arg Lys Ala Glu Glu Ser Glu Lys Lys Ala Ala Glu
350 245 250 255
352 Ala Lys Gln Lys Val Asp Thr Lys Glu Gln Gly Lys Pro Lys Arg Arg
353 260 265 270
355 Ala Lys Arg Gly Val Ser Gly Glu Leu Ala Thr Pro Asp Lys Lys Glu
356 275 280 285
358 Asn Asp Ala Lys Ser Ser Asp Ser Ser Val Gly Glu Glu Thr Leu Pro
359 290 295 300
361 Ser Pro Ser Leu Asn Ala Met Ala Asn Glu Ser Gln Thr Glu His Arg
362 305 310 315 320
364 Lys Asp Val Asp Glu Tyr Ile Lys Lys Met Leu Ser Glu Ile Gln Leu
365 325 330 335

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09/298523A 6

Thr Gly Trp Leu Gln Ser Trp Tyr Tyr Leu Asn Asn Gly
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Asp Met Ala

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<211> LENGTH: 21

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pneumoniae

<400> SEQUENCE: 24

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<211> LENGTH: 20

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pneumoniae

<400> SEQUENCE: 25

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Gly Ala Leu Ala
20

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<211> LENGTH: 18

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pneumoniae

<400> SEQUENCE: 26

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1 5 10 15
Val Asn

<210> SEQ ID NO 27

<211> LENGTH: 20

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pneumoniae

<400> SEQUENCE: 27

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1 5 10 15
Gly Ala Met Ala
20

<210> SEQ ID NO 28

<211> LENGTH: 20

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pneumoniae

<400> SEQUENCE: 28

Thr Gly Trp Leu Gln Xaa Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn
1 5 10 15
Gly Ala Met Ala
20

see item 10 on Eva Summary Sheet

<210> SEQ ID NO 29

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pneumoniae

<400> SEQUENCE: 29

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1 5 10 15
Val

<210> SEQ ID NO 30

<211> LENGTH: 20

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pneumoniae

<400> SEQUENCE: 30

FYI:

Please Note:

Use f n and/or Xaa have been detected in the Sequence Listing. Please review the S quence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

DATE: 11/16/2000

PATENT APPLICATION: US/09/298,523A

TIME: 18:17:03

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Output Set: N:\CRF3\11162000\I298523A.raw

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L:1664 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:28
L:3795 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:71
L:3795 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:71
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L:3927 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:74
L:3927 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:74
L:3927 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:74
L:3927 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:74
L:3927 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:74